

Figure 1
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MOTTQESCPGSEFDTEDGWEFJLCRGEJNFGCGSGKKRGKFVKVFESEAPSVIDELLLTEWHLFAPNLVVS1VGEERPLAMKSWLRDVLF
KGLVKRAQESTGAWIJLTSALHVGЛАKHWGCAVKDHSLAESTETKJFVVAJGMASLDHJLHKQOLLDCVHQKEDTPJHYPADEGN1QGPLCPI
LENLSEHJLVESGALGSGNDGILTELQLEKHISEQRTGCGTSC10JFVLCLLNGDPNTLERK15FAVEQAAWPWLJAGSGGJADVL
ALVSQPHLLVPIQVAEKOFREKFFSECFSWEAJVHWTELLQNJAHFHLLTVYDFQEGSEEDLDTVJLKAJLVACKSHSQAQDYLDEL
LAVAWDKVJIAKSEJFNGDVEWKSCDLEEVMTDALVSNKFDFVLFVDSGADMALFLTYGRQOGLYHSVSPKSLLFELLORKHEEGRL
LAGLGAGQCAKELPFIJGLFAFSLHVEKVLKDFLHDACFGFYQDGRKMEEGFFKRFAGOKWLFD15EKKSEDPWRLDFLWAVLQNYEMATY
TWAMCFEGVAAALACKJIKEMSHLIEKAIEVAKTMRREAKYEQALALISECYGNSEDKAFALLVKNHSWSRTTCLHlateADAKAFFA
HDGVQAFLTKJWWGDMATGTJPLKLIGAFTCHALITYTNLJSFSEDAPQHMLEDLQEPFDELDMEKSTLCEFRGGQOLEKLTAPRAPGDLC
FOAAFLLTREWWKFWGAFVTVFVFLGNVVMYTAFLFLFTYVLLVDFRFPQGJSGSEVTLYFWVFTLVLEEJFQGFFTDDETHLVKKFTLYV
EDRNWKCDMVAJFLFJVGVTCKMVPSEVFLAGKTVLAJDFMVFTLKLJHJFAJHKQLGPKJJVERMMKDVFVFFLFLSVWLVAYGVTT
ALLHFDHGKLEWJFKVLYKFLYJFGQJFLDEJDEARVNCSLHPLLSEASCNPNLYANWLVIJLLVTFLVTNVLLMNLLIAMFSYJ
FQVVOQNAADMFTWKFQRYHLJVEYHGRPAJAPPFILLSHL15LVLKQVFKKEAOKHKGHLERDLPDFLDQKJITWETVQKENFLSTMEKRF
RDSEGEVLRKTAHVDLJAKYJGGLECEKKJKCLESANCMLLSSMTD1APGGTYSSSONCGCRSOPASARDREYLESGLPPSDT

Figure 2
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Human TFRt nucleotide sequence

SEQ New: 3498 bp;

Composition: 634 A; 1089 C; 1143 G; 632 T; 0 OTHER

Percentage: 18% A; 31% C; 33% G; 18% T; 0% OTHER

Molecular weight (kDa): ssDNA: 1081.34 dsDNA: 2157.1

ORIGIN

1 ATGCAGGATG TCCAAAGCCCC CCGTCCCCGA AGCCCCCGGG ATGCTGAAGA CCGGGCGGGAG
2 CTGGGCTTGC ACAGGGCGA GGTCAACTTT GGAGGGCTG CGAAGAAGCG AGGCAAGTTT
3 GTACGGGTGC CGAGCGGAGT GGGCCCGTCT GTGCTCTTTC ACCTGCTGCT TGCTGAGTGG
4 CACCTGCCGG CCCCCAACCT GGTGGTGTCTC CTGGTGGCTG AGGAGCAGCC TTTCGCCATG
5 AGTCTCTGGC TCCGGGATGT CTGGGGCAAG GGGCTGGTGA AGGCGGCTCA GAGCACAGGA
6 GCCTGGATCC TGACCAAGTGC CCTCCCGCTG GGCCTGGCCA GGCAATGTCGG GCAGGGCGTGG
7 CGCGACCACT CGCTGGCCAG CACGTCCACC AAGGTCCCTG TGGTTGCTGT CGGCATGGCC
8 TCGCTGGGCC GCGTCCTGCA CGGCCGCAATT CTGGAGGAGG CCCAGGAGGA TTTTCCGTG
9 CACTACCCCTG AGGATGACGG CGGCAGCCAG GGCCCCCTCT GTTCACTGGA CAGCAACCTC
10 TCCCACATTCA TCCTGGTGGA GCCAGGCCCC CGGGGGAAAGG GCGATGGGCT GACGGAGCTG
11 CGGCTGAGGC TGGAGAAGCA CATCTCGGAG CAGAGGGCGG GCTACGGGGG CACTGGCAGC
12 ATCGACATCC CTGTCCTCTG CTGCTGGTCA AATGGTGTATC CCAACACCTT GGAGAGGATC
13 TCCAGGGCCG TGGAGCAGGC TGCCCCGTGG CTGATCCCTGG TAGGCTCGGG GGGCATCGCC
14 GATGTCCTTG CTGCCCTAGT GAACCAGGCC CACCTCTGG TGCCCAAGGT GGCGAGAAAC
15 CAGTTTAAGG AGAAGTCTCC CAGCAAGCAT TTCTCTGGG AGGACATCGT GCGCTGGACCC
16 AAGCTCTGC AGAACATCAC CTCACACCCAG CACCTGCTCA CCCTGTATGA CTTCGAGCAC
17 GAGGGCTCCG AGGAGCTGGA CACGTCATC CTCAAGGCC TGCTGAAAGC CTGCAAGAGC
18 CACAGCCAGG AGCCTCAGGA CTATCTGGAT GAGCTCAAGC TGGCCGTGGC CTGGGACCCGC
19 GTGGACATCG CCAAGAGTGA GATCTTCAT GGGGACGTGG ACTGGAAGTC CTGTGACCTG
20 GAGGAGGTGA TGGTGGACGC CCTGGTCAAGC AACAAAGCCCG AGTTGTGCG CCTCTTGTG
21 GACAAACGGCG CAGACGTGGC CGACCTCTG ACGTATGGG GGCAGCAGGA GCTCTACCGC
22 TCCGTGTCAC GCAAGAGCC TCTCTTCGAC CTGCTGAGC GGAAGCAGGA GGAGGCCCGC
23 CTGACGCTGG CGGGCTGGG CACCCAGCAG GCCCCGGAGC CACCCGCGGG GCCACCGGCC
24 TTCTCCCTGC ACCAGGTCTC CGCCGTACTC AAGGACTTCC TGCAAGCACG CTGCCGAGGC
25 TTCTTACCAAGG ACGGCCGGCC AGGGGACCGC AGGAGGGCGG AGAAGGGCCC GGCAAGAGC
26 CCCACGGGCC AGAAGTGGCT GCTGGACCTG AACCAAGAAGA GCGAGAACCC CTGGCGGGAC
27 CTGTTCTGT GGGCCGTGCT GCGAAGACCGC CACGAGATGG CCACCTACTT CTGGGCCATG
28 GGCAGGAAAG GTGTGGCAGC CGCACTGGCC GCCTGCAAAA TCTCTAAAGA GATGTCGCAC
29 CTGGAGACGG AGGCCGAGGC GGCCCAGGCC ACGCGCAGG CGAAATACGA GCGGCTGGCC
30 CTTGACCTCT TCTCCGAGTG CTACAGCAAC AGTGAGGGCC GCGCCTTCGC CCTGCTGGTG
31 CGCCGGAAAC GCTGCTGGAG CAAGACCAAC TGCCCTGCACC TGCCACCGA GGCTGACGCC
32 AAGGCCTTCT TTGCCACGA CGGGCTTCAG GCCTTCTGCA CCAGGATCTG GTGGGGGGAC
33 ATGGCCGAG GCACGCCAT CCTGCGGCTG CTAGGAGCCT TCCCTGCCCC CGCCCTCGTC
34 TATACCAACC TCATCACCTT CAGTGAGGAA GCTCCCTGA GGACAGGCCT GGAGGACCTG
35 CAGGACCTGG ACAGCCTGGA CACGGAGAAG AGCCCGCTGT ATGGCCTGCA GAGCCGGGTG
36 GAGGAGCTGG TGGAGGCAGC GAGGGCTCAG GGTGACCGAG GCCCACGTGC TGTCTCTG
37 CTCACACGCT GGCAGAAATT CTGGGGCGCT CCCGTGACTG TGGTCTGGG GAACGTGGTC
38 ATGTAACCTG CCTTCCTCTT CCTGTTCAAC TACGTCCTGC TGGTGGACTT CAGGCCGCC
39 CCCAGGGCC CCTCAGGGCC CGAGGTCAAC CTCTACTTCT GGGTCTTTAC GCTGGTGCTG
40 GACCAAAATCC GGCAGGGCTT CTTCACAGAC GAGGACACAC ACCTGGTGA AAAGTCACA
41 CTCTATGTGG GGGACAACGTG AAACAAGTGT GACATGGTGG CCATCTTCCT GTTCATCGTG
42 GCTGTCACCT GCAGGATGCT GCCGTCGGCG TTTGAGGCTG GCCGCACGGT CCTCGCCATG
43 GACTTCATGG TGTTCACGCT CGGGCTGATC CATATCTTG CCATACACAA GCAGCTGGGC
44 CCCAAGATCA TCGTGGTAGA GCGCATGATC AAGGACGTCT TCTTCTTCCT CTTCTTCTG
45 AGCGTGTGGC TCGTGGCTA CGGTGTCACC ACCCAGGCC TGCTGCACCC CCATGACGGC
46 CGCCTGGAGT GGATCTCCG CCGGGTGTCT TACCGGCCCT ACCTGCAAGAT CTTCGGCCAG
47 ATCCCCACTGG ACGAGATTGA TGAAGCCCCGT GTGAACTGCT CCACCCACCC ACTGCTGCTG
48 GAGGACTCAC CATCCTGCC CAGCCTCTAT GCCAAGTGGC TGGTCATCCT CCTGCTGGTC
49 ACCTTCTGT TGGTGAGGAA TGTGGTGTCTC ATGAACCTGC TCATCGCCAT GTTCAGCTAC
50 ACGTTCCAGG TGGTGCAAGG CAACGCAAGAC ATGTTCTGGA AGTTCCAGCG CTACAACCTG

Figure 3A
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301 ATTCTGGAGT ACCACCAACCG CCCCCGCCCTG GCCCCGCCCT TCAATCCTGCT CAGCCACCTG
302 AGCCCTGAGCG TCCCGCCGGGT CTTCAAGAAG GAGGCTGAGC ACAAGCGGGGA GCACCTGGAG
303 AGAGACCTGC CAGACCCCCCTG GACCCAGAAG CTCTCTACCTG GGGAGAGAGT CCAGAGGGAG
304 TACTTCCTGA GCAAGATGGGAA GAAAGCCGAGG AGCCGACACCC AGGGGGGAGGT GCTGCCGAAG
305 ACCGGCCACA GAGTCGACTT CATTGCCAAG TACCTCTTGGG GGCTGAGAGA GCAAGAAAAAG
306 CGCATCAAGT GTCTCGACTC ACAGATCAAC TACTCTCTCGG TGCTCGTGTGTC CTCCGTGGCT
307 GACCTGCTGG CCCAGCTGG CGGCCCCCCCCGG AGCTCTCAGG ACTCTGGCGA GGGAAAGCCAG
308 CTGGTGGCTG CTGACCAACAG AGGTGGTTTA GATGGCTGGG ACAAAACCCGG GGCTGGCCAG
309 CCTCCCTCGG ACACATGA

Figure 3B
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Human TRF1 protein coding sequence
Translation of Htrpb coding (1-3498)
Universal code
Total amino acid number: 1165, MW=131281
Max ORF: 1-3498, 1165 AA, MW=131281

ORIGIN

1 M0DVQGPRPG SPGDAEDRRE LGLHAGEVNF GGSCKKRGKF VRVPSCVAP*
2 VLFDLILLAEW H1FAFNLVVS 1VGEEQFFAM KSWLRDVLRK GLVKAQSTG
3 AWIILTSALRV GLAKHVGQAV RDHCLASTST KVRVVAVGMA SLGRVLHRRK
4 LEEAQEDFPV HYPEDDGGSO GPLCSLDENL SHF1LVEPGP PGKGDGLTEI
5 RLFLERKHISE QRAYGGTGS 1E1FVLCLLIV NGDPNTLERI SRAVEQAAPK
6 L1LVGSGG1A DVAALVNQF HLLVPKVAEK QFKEKFPSKH FSWEDIVRWI
7 KLLQNIITSHQ HLLTVYDFFQ EGSEELDTVI LKALVKACKS HSQEPQDYLI
8 ELKLAVAWDA VDIAKSEJFN GDVEWKSCDL EEVMDALVS NKPEFVRLFV
9 DNGADVADFL TYGRLQELYR SVSRKSELLFD LLQRKQEEAR LTLAGLGTQO
10 AREFFAGFFA FSLHEVSRVL KDFLQDACPQ FYQDGRPGDR RRAEKGPAKF
11 PTGOKWLLDL NOKSENFWRD LFLWAVLQNF HEMATYFWAM GQEGVAAALA
12 ACK1LKEMSH LETEAEAAARA TREAKYERLA LDLFSECYSN SEARAFALLV
13 RENRCWSKTT C1HLATEADA KAFFAHDGVQ AFLTRIWWGD MAAGTPILRL
14 LGAFLCPALV YTNLITFSEE AFLRTGLEDL QDLDSDLTEK SPLYGLQSRV
15 EELVEAPRAQ GDRGPKAVFL LTRWRKFWGA PVTVFLGNVV MYFAFLFLFJ
16 YVLLVDFRPP PQGPGSGFETV LYFWVFTLVL EElRQGFFTD EDTH1VKKFT
17 LYVGDWNWNC DMVAJFLF1V GVTCKMLPSA FEAGRTVLAM DFMVFTLRLJ
18 H1FAJHKQLG PK11VVERMM KDVFFFLLFV SWLVAYGVT TOALLHPHDG
19 ELEW1FRRVL YRPYLOI1FGQ 1PLDE1DEAR VNCSTHPLLL EDSPSCPSLY
20 ANWLV1LLV TFL1VTNVLL MNLL1AMFSY TFOVVQGNAD MFWKFORYNL
21 IVEYHEP1AL APPF1LLSHL S1T1KRVFKK EAEHKREHLE RDLPDPLDQY
22 VVTWETVQKE NFLSKMEKRR RDSEGEVLRK TAHRVDFIAK YLGGLREQEK
23 R1KCLESQIN YCSV1VSSVA DVLAQGGGPR S5QHCGEGSQ LVAADHREGGI
24 DGWEQPGAGQ PPSDT*

Figure 4
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FIGURE 1. Comparison of the amino acid sequences of mouse and human TSH.

Figure 5
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Classification and Secondary Structure Prediction of Membrane Protein

<http://azusa.proteome.bio.tuat.ac.jp/sosui/>

Orientation of the N-terminus of mTrp6: IN

Number of transmembrane helices of mTrp6: 6

Position of transmembrane helices of mTrp6:	helix	begin	end
1	731	754	
2	769	791	
3	807	829	
4	839	861	
5	870	891	
6	959	971	

Orientation of the N-terminus of hTrp6: IN

Number of transmembrane helices of hTrp6: 6

Position of transmembrane helices of hTrp6:	helix	begin	end
1	732	751	
2	770	791	
3	807	829	
4	843	861	
5	873	891	
6	959	971	

Figure 6A
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Hydropathicity profile of mTrp8 (Made with DNAMAN software)

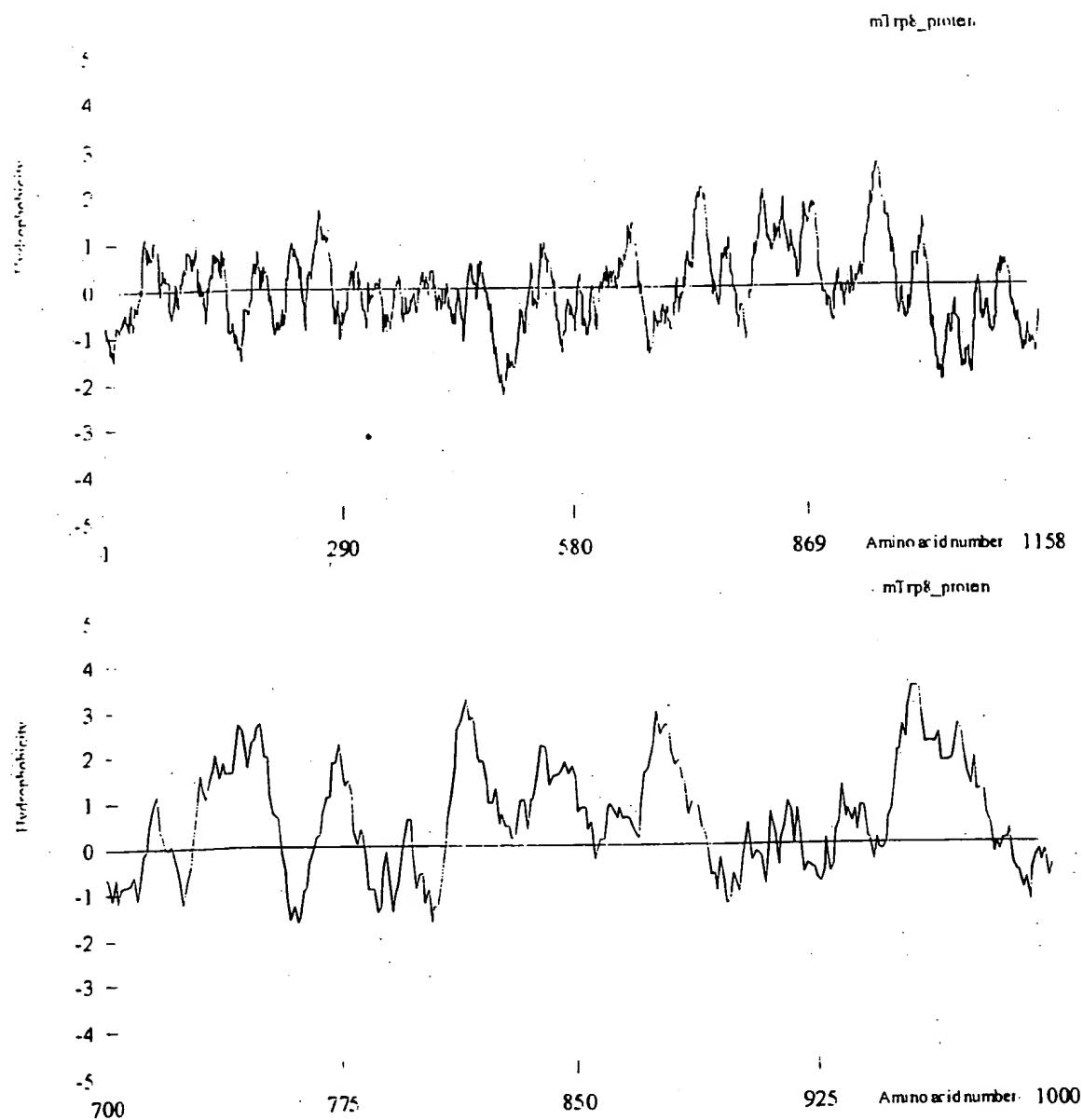


Figure 6B
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Hydrophobicity profile of hTrpE (Made with DNAMAN software)

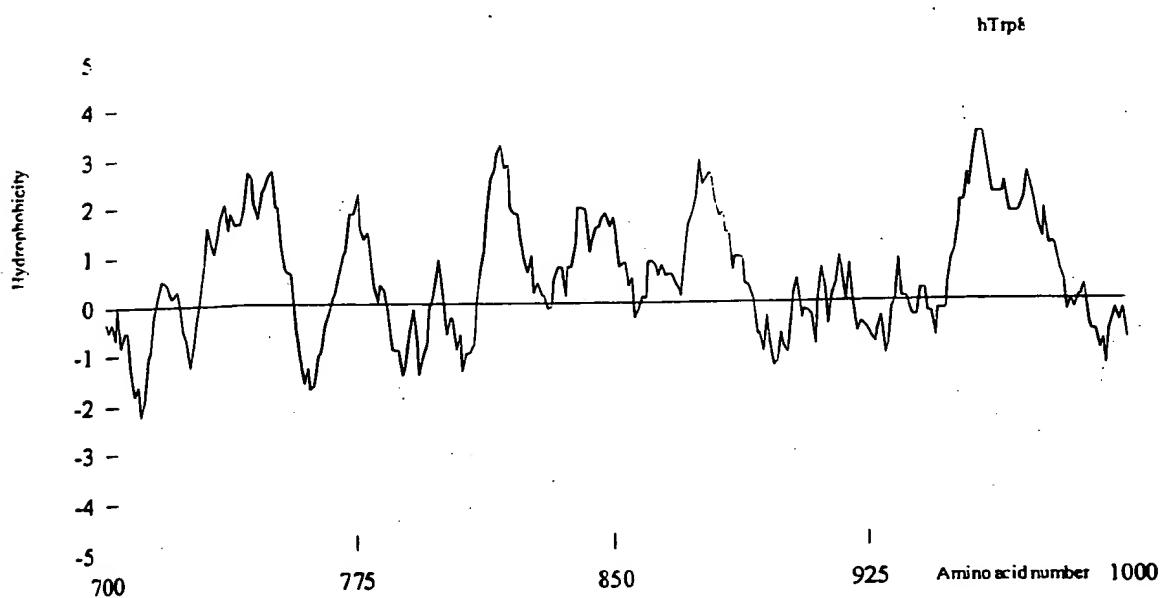
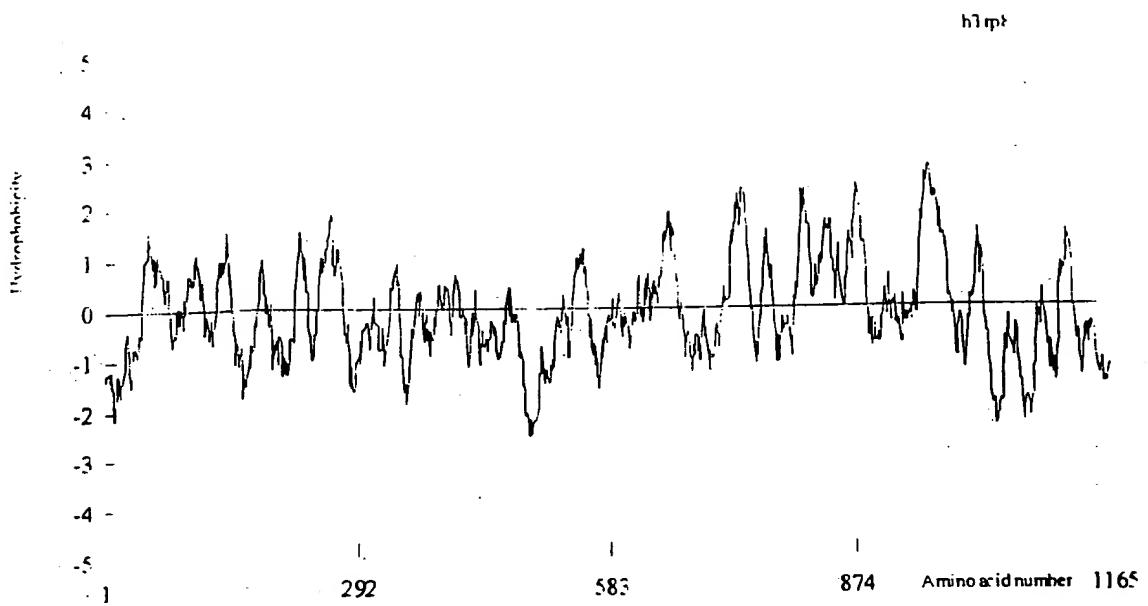


Figure 6C
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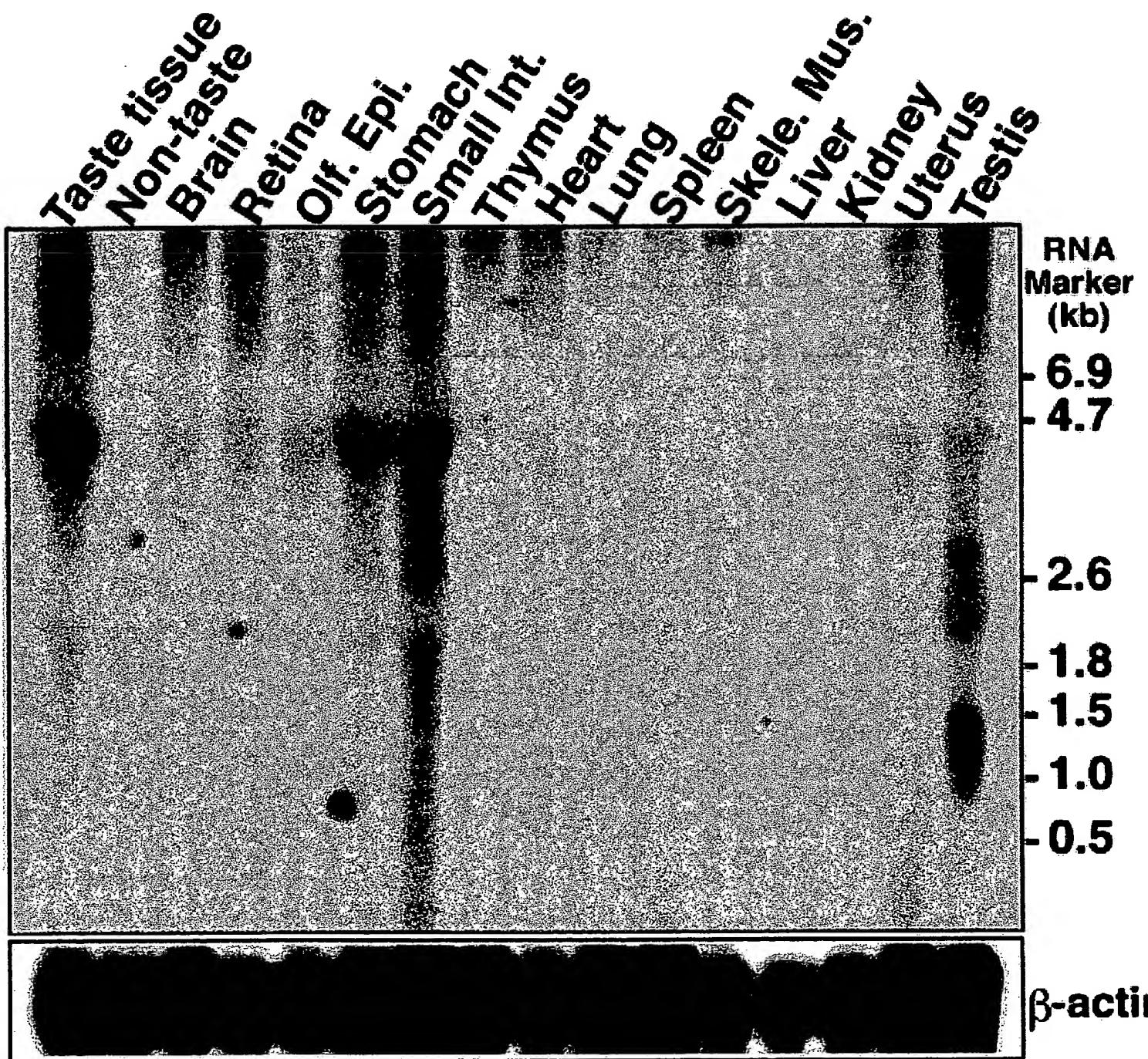


Figure 7
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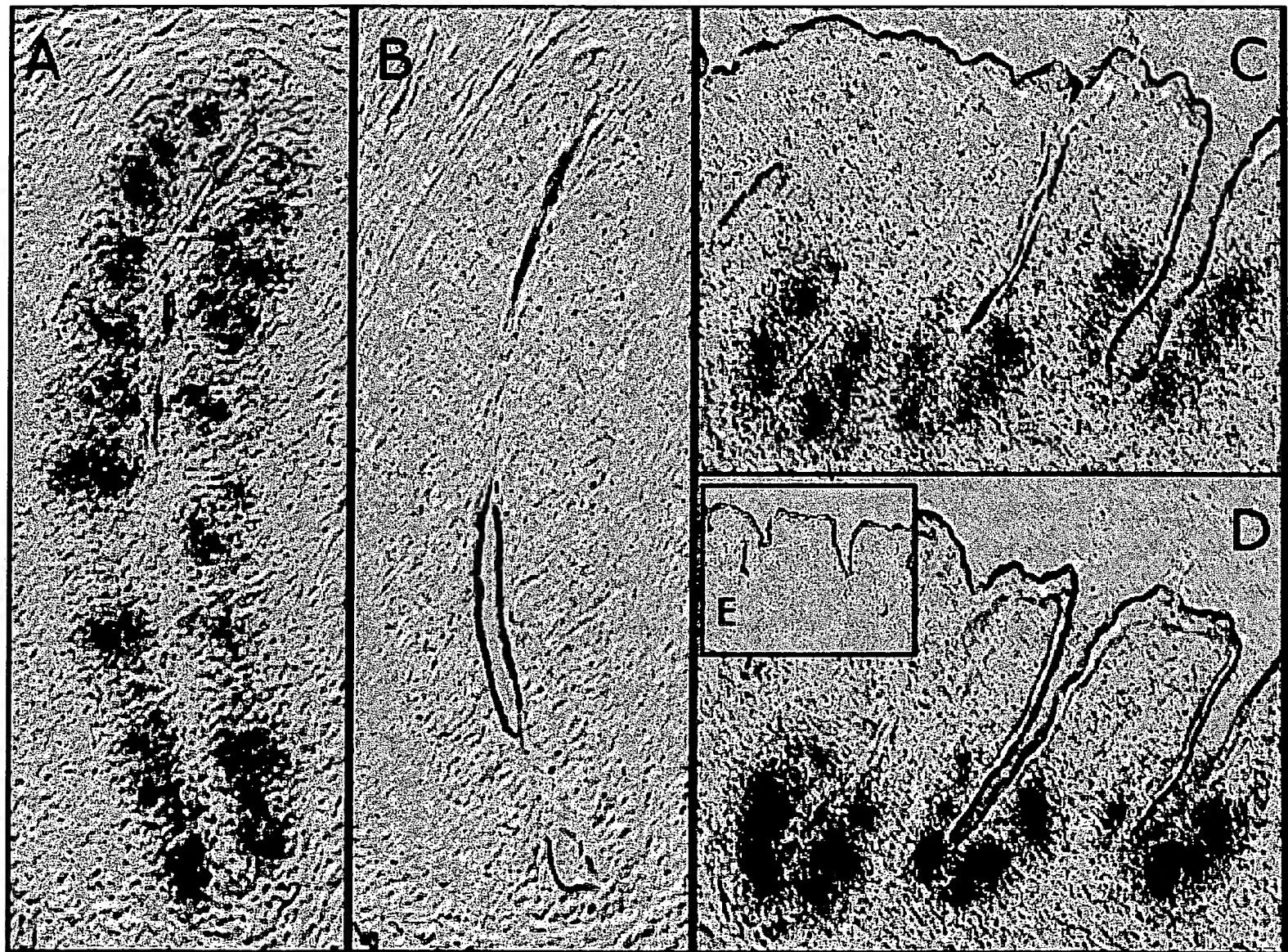


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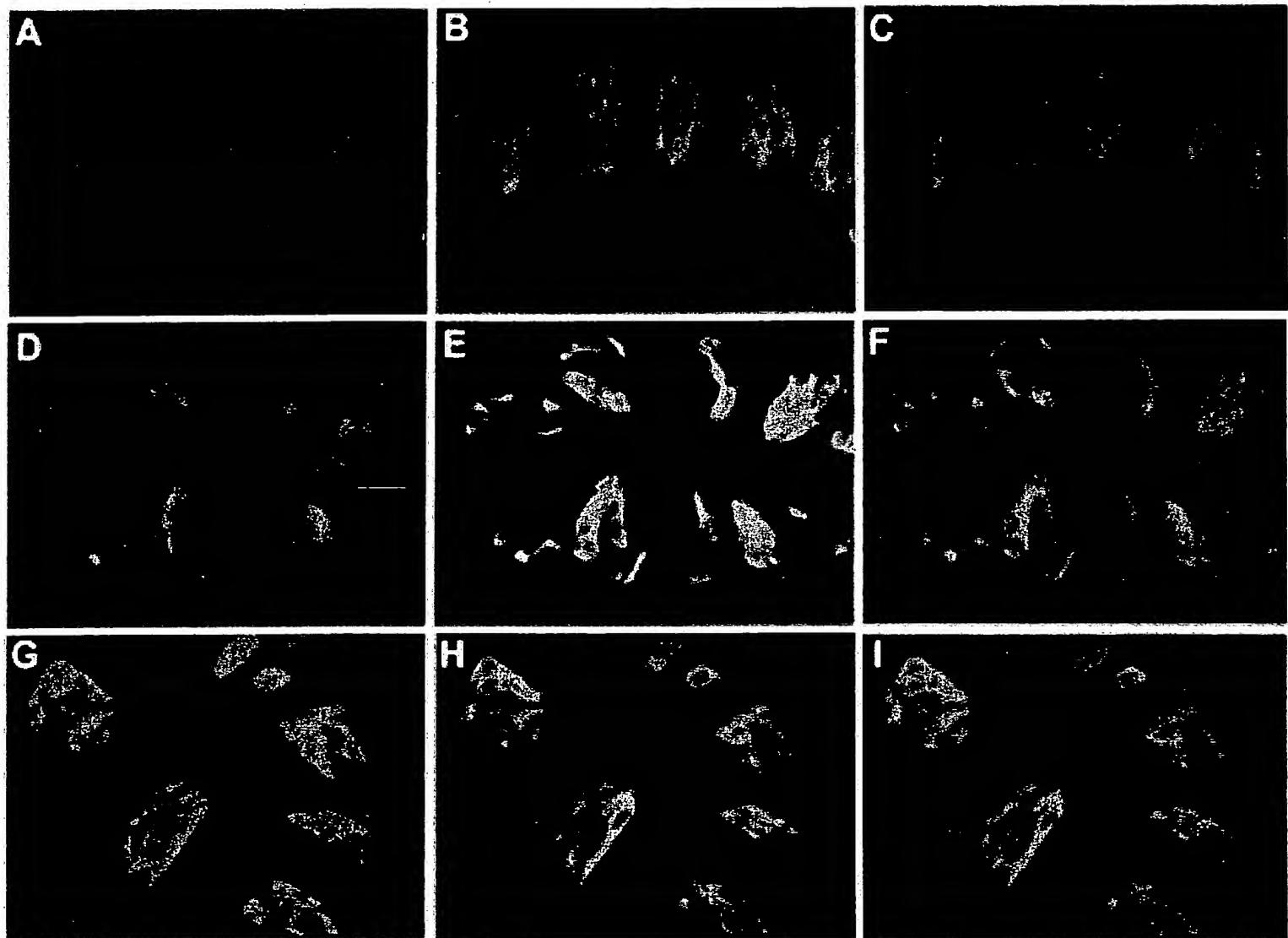


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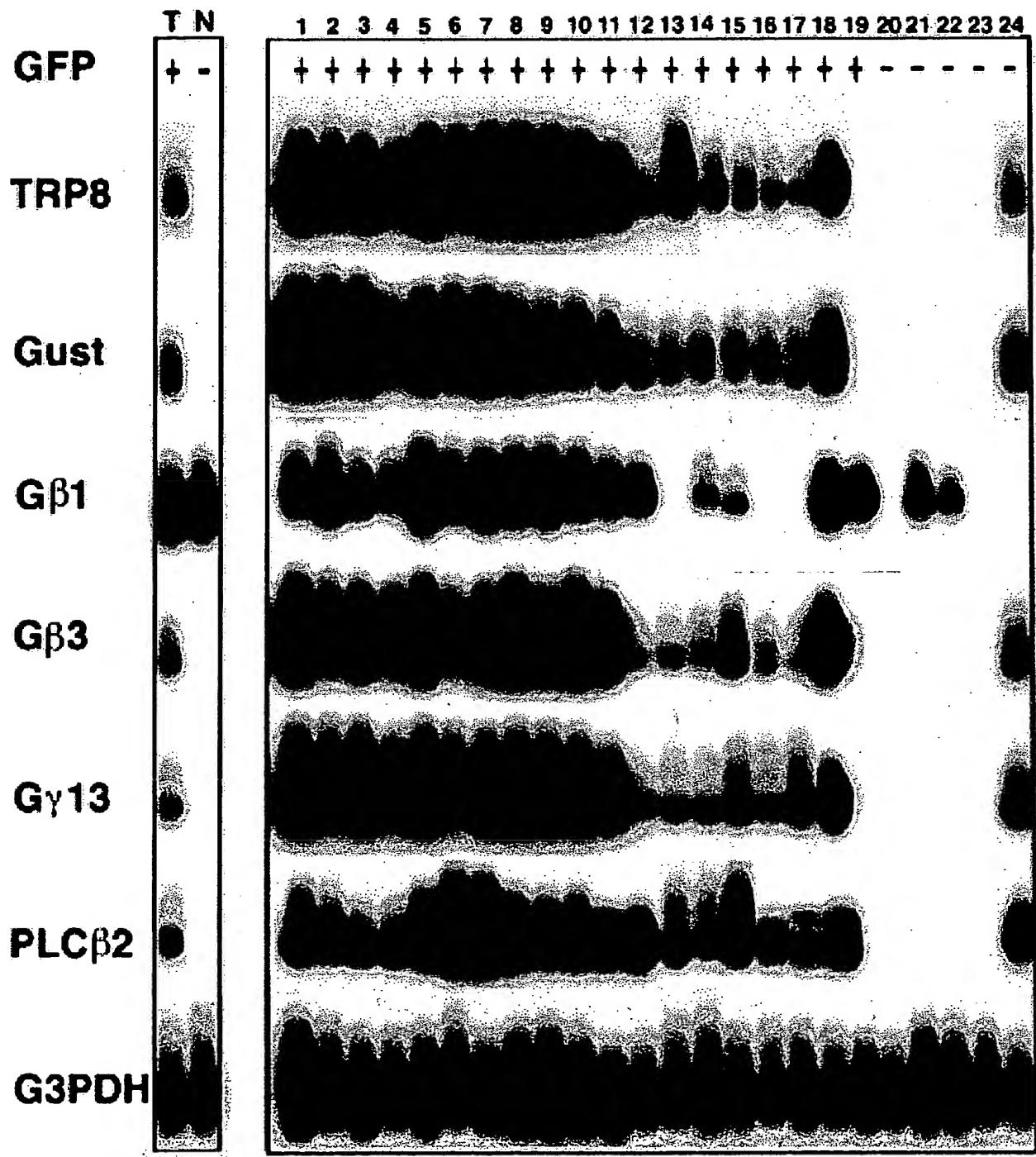


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Taste
Brain

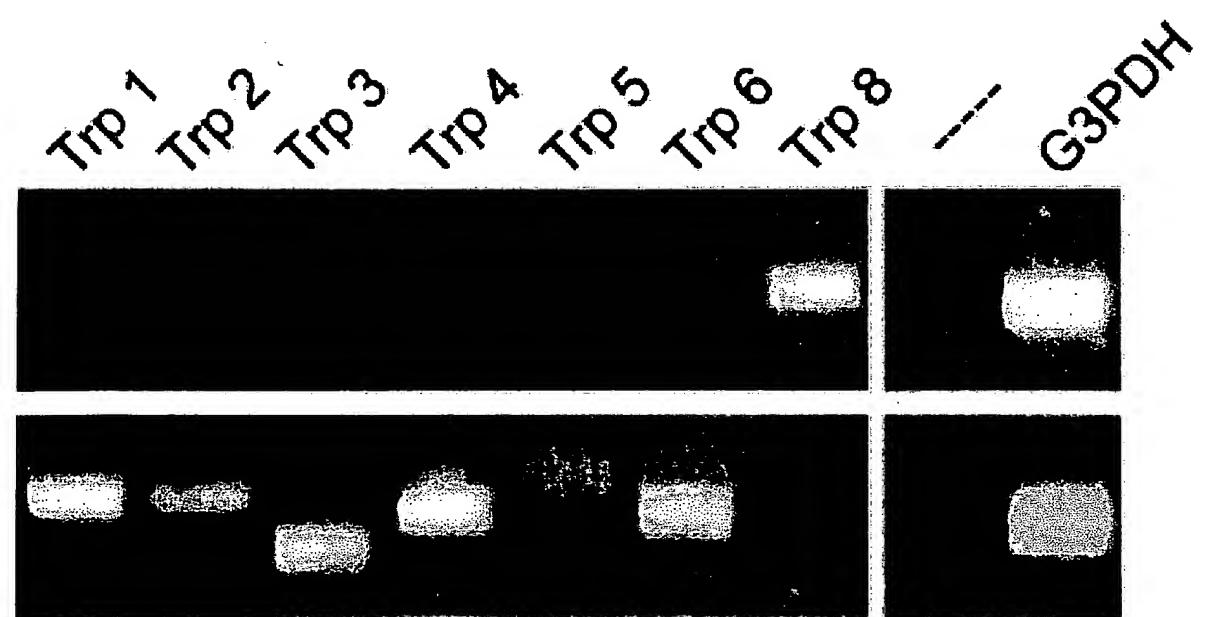
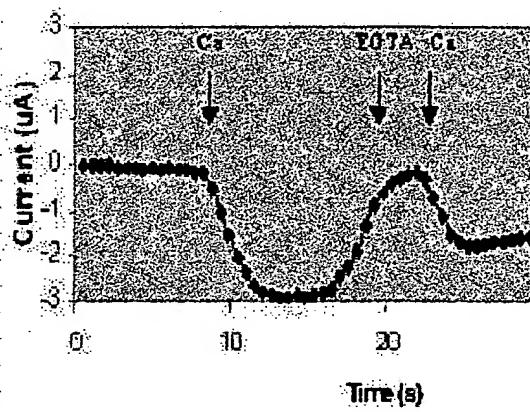
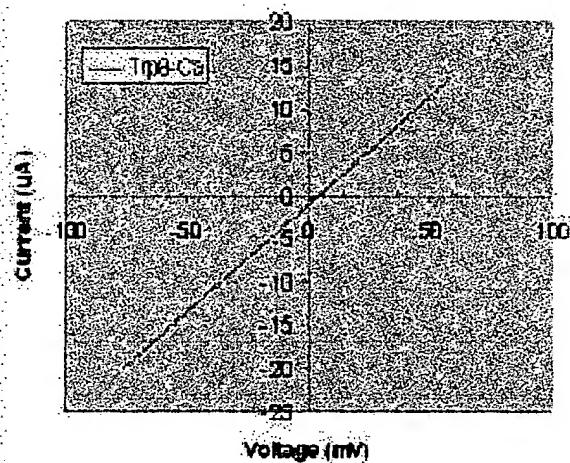


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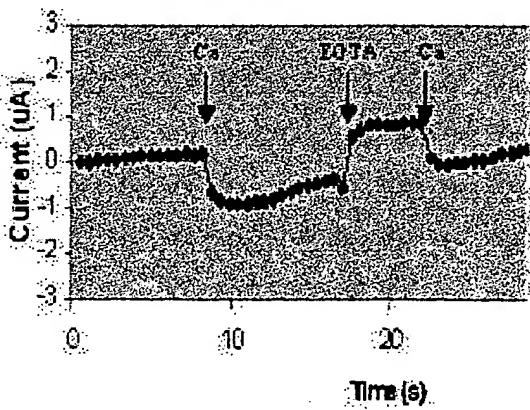
Trp8 + Thapsigargin



I-V Relationship in Trp8-injected oocytes



H2O + Thapsigargin



PeakI_{Ca}

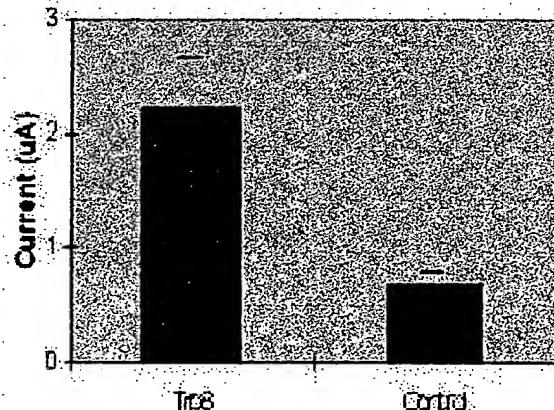


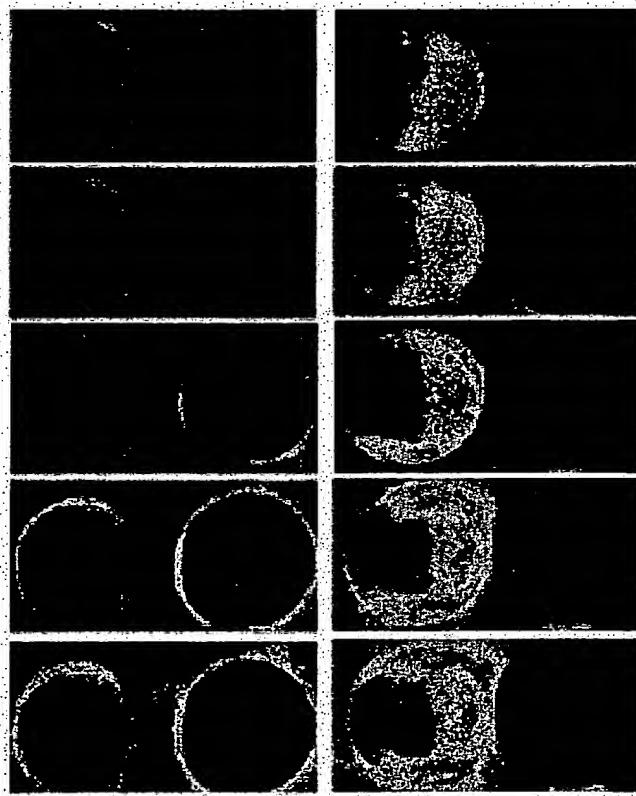
Figure 12
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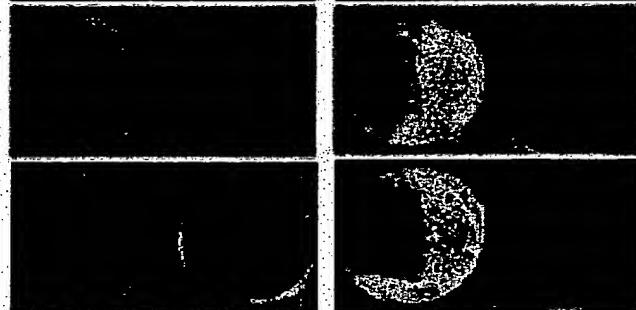
Injected with: **H₂O** **TRP8 cRNA**

Thapsigargin 2uM: + - + -

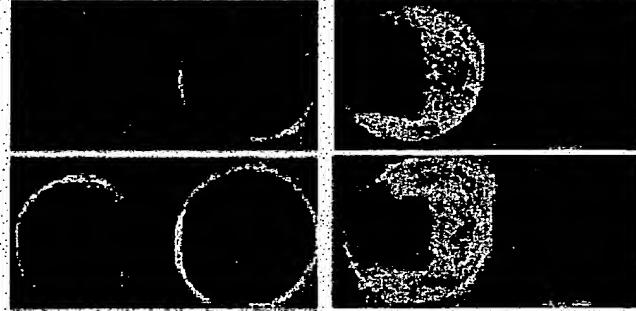
0 s after Ca-addition:



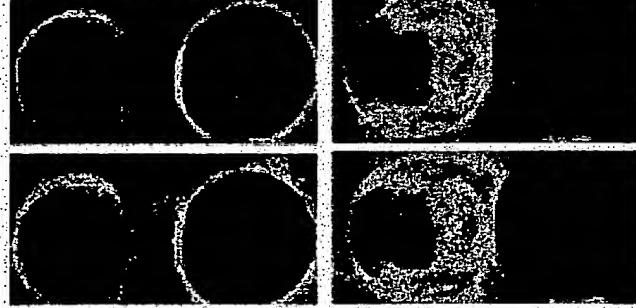
25 s after Ca-addition:



50 s after Ca-addition:



75 s after Ca-addition:

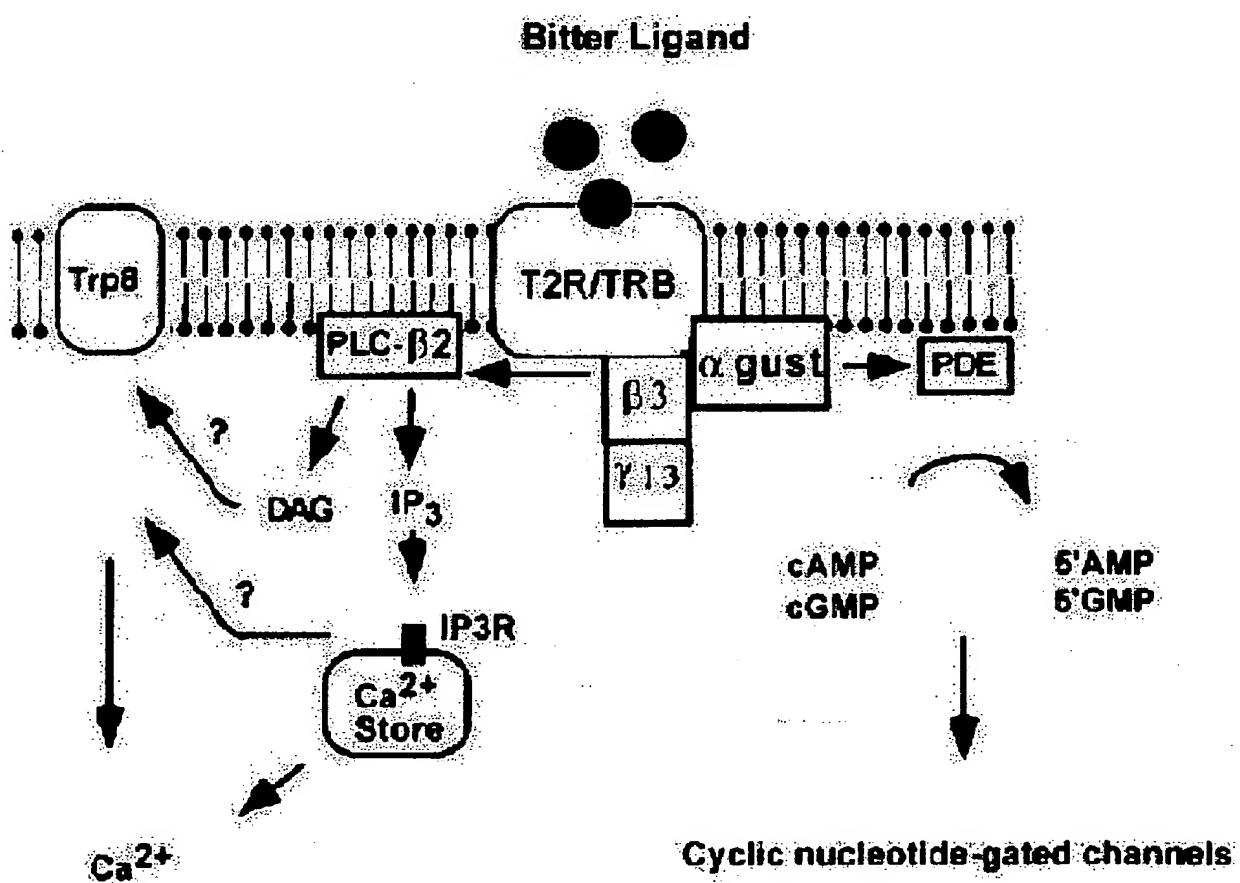


100 s after Ca-addition:



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Transduction of Taste Stimuli



Modified from Kinnamon, *Neuron* (2000) 25:507-510

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